

# Hydrogenomics of the Extremely Thermophilic Microorganism *Caldicellulosiruptor saccharolyticus* for Bioenergy Production



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# Biohydrogen

## Types of Biomass

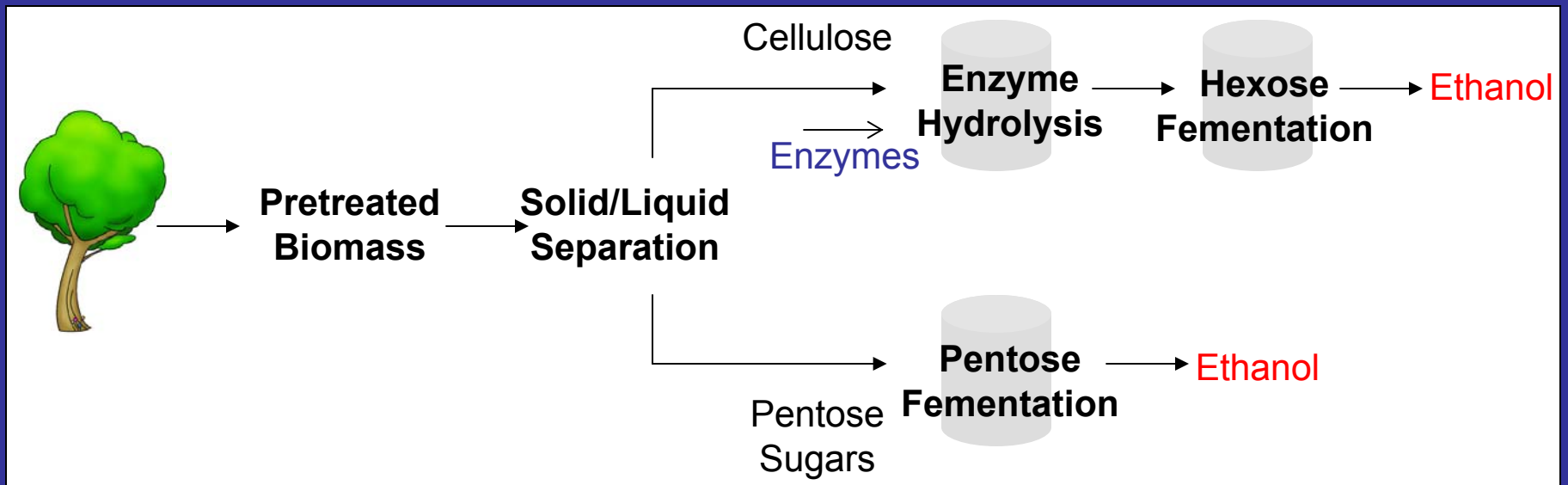


Switchgrass



Poplar

- Sources of cellulose more abundant than corn



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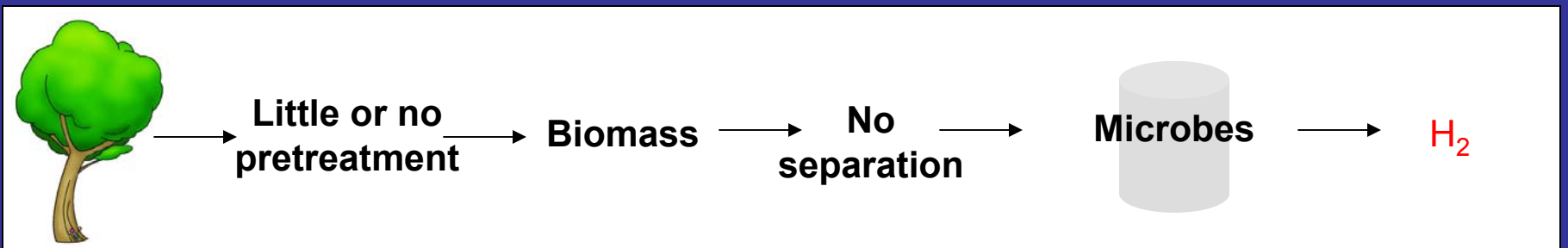
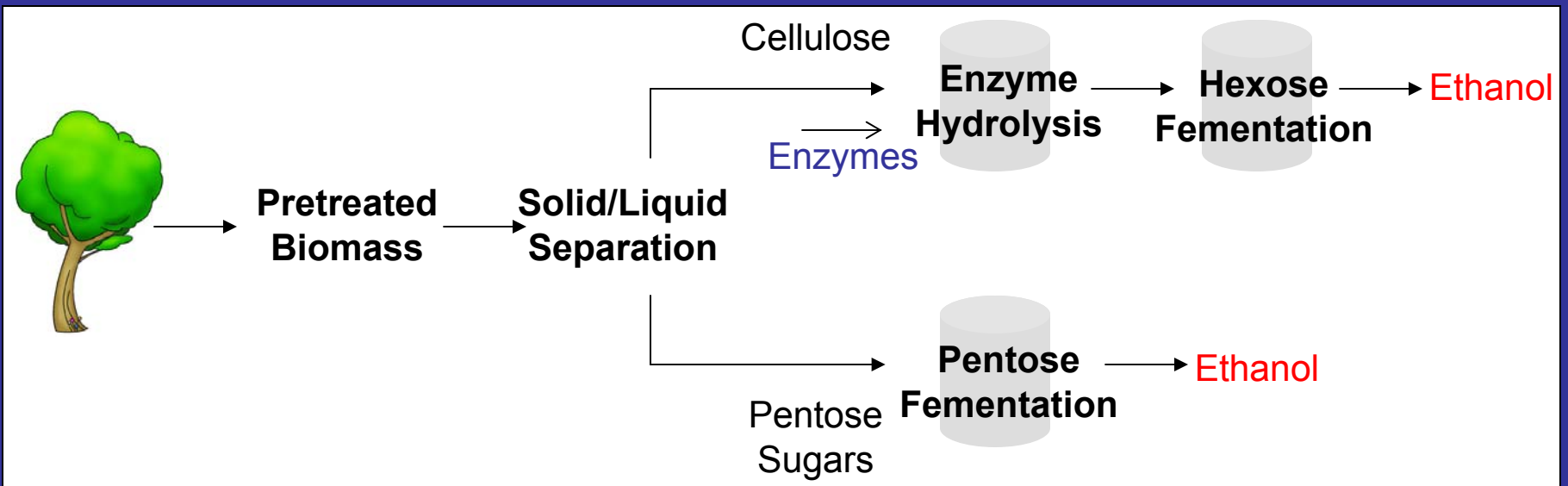


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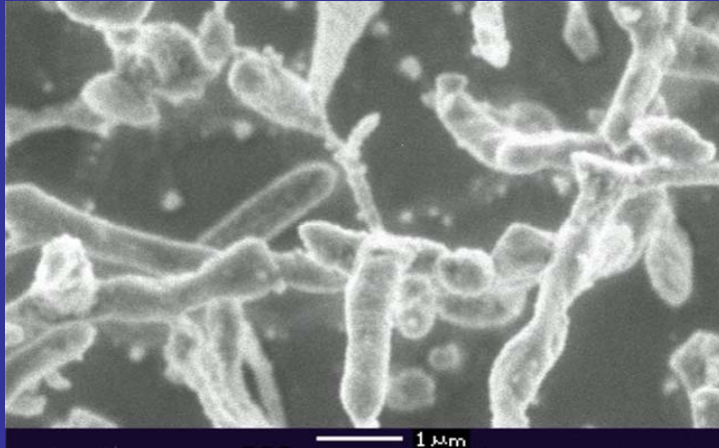


Poplar

- Sources of cellulose more abundant than corn



# *Caldicellulosiruptor saccharolyticus*



Downstream from a 78°C pool

$T_{\text{opt}} = 70^{\circ}\text{C}$

Fermentative heterotroph

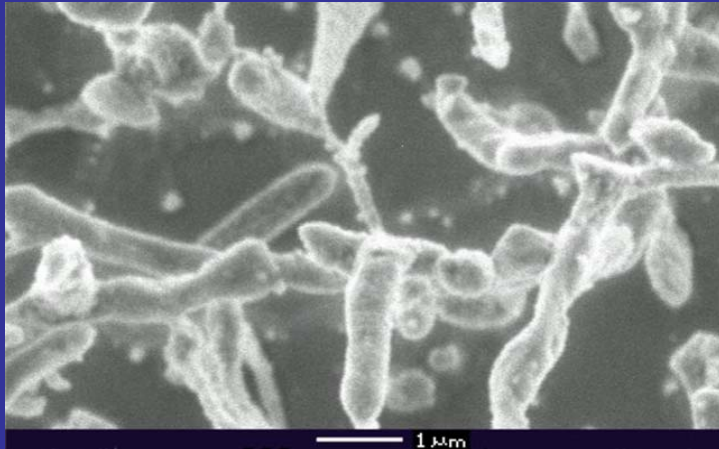
Bacterium

Rod-shaped

Asporogenous

Produces  $\text{H}_2$   
acetate, lactate,  $\text{CO}_2$  and  
ethanol

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## Oligo/Monosaccharides

### Grows on:

Cellobiose  
Fructose  
Galactose  
Glucose  
Lactose  
Maltose  
Rhamnose  
Xylose

### Does not grow on:

Sorbitol  
Raffinose  
Ribose  
Sorbitose

## Polysaccharides

### Grows on:

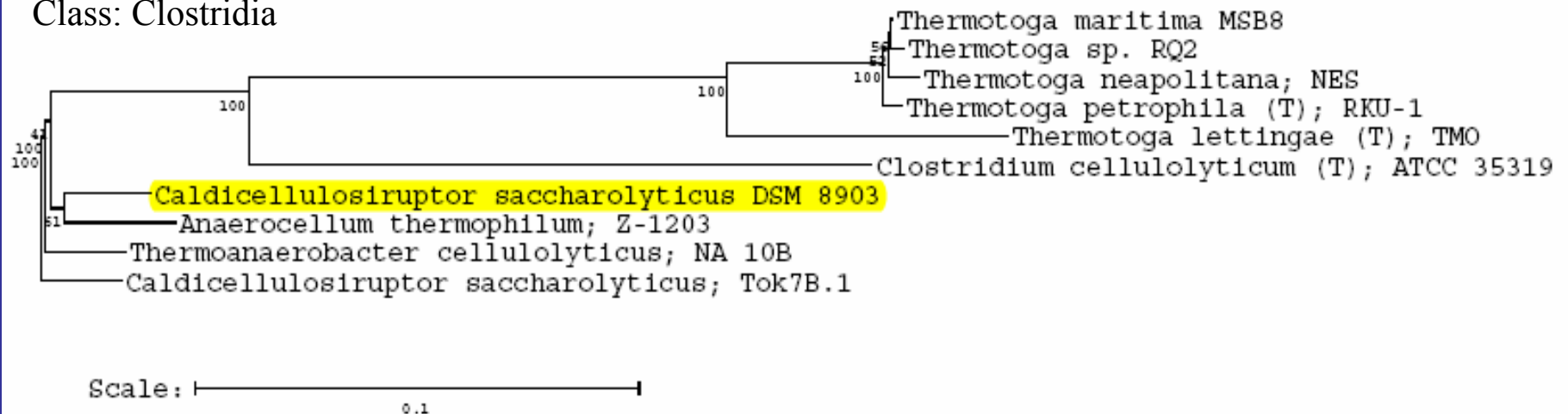
Cellulose (Avicel)  
Starch  
Pullulan  
Laminarin  
Lichenin  
Pectin  
Xylan

### Does not grow on:

Inulin  
Glycogen

# *Caldicellulosiruptor saccharolyticus*

Class: Clostridia

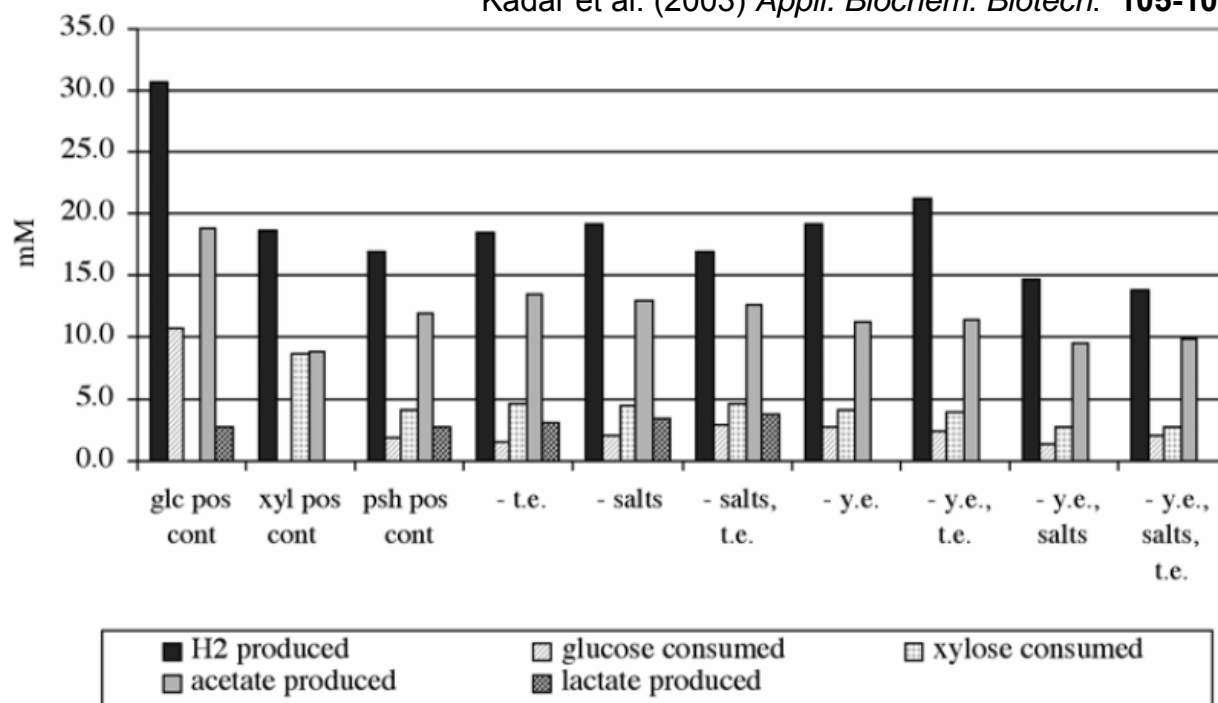


- Thermophiles offer many advantages over mesophiles
  - Increased solubility of substrates
  - No problems with sulfate reducers and methanogens
  - Fewer fermentative byproducts
  - Approach Thauer limit:  $4\text{H}_2$  / glucose

# BioH<sub>2</sub> Production by *Csac*

Grows on waste paper hydrolysate

Kadar et al. (2003) *Appl. Biochem. Biotech.* **105-108** 557-66.

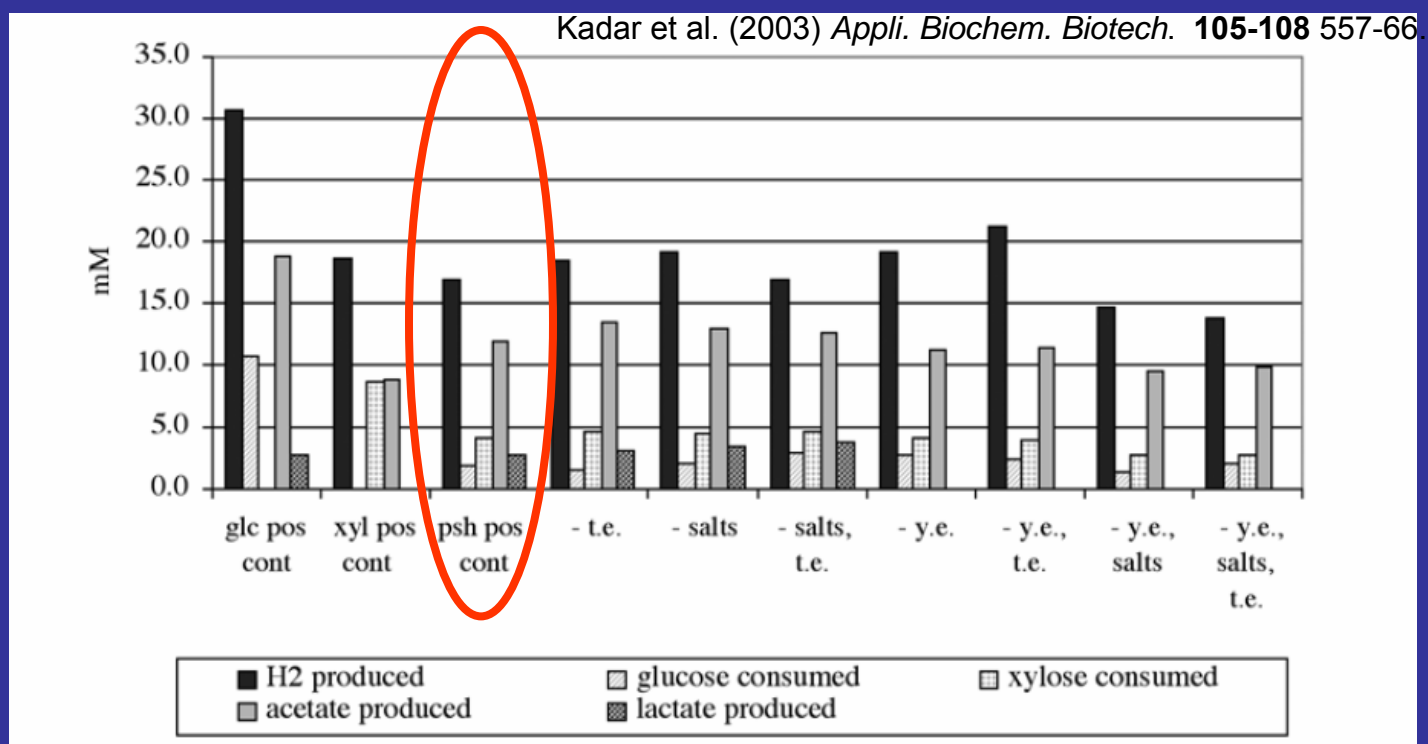


Higher tolerance H<sub>2</sub> than other thermophiles

# BioH<sub>2</sub> Production by *Csac*

Grows on waste paper hydrolysate

- Co-ferments xylose and glucose
- Xylose > Glucose

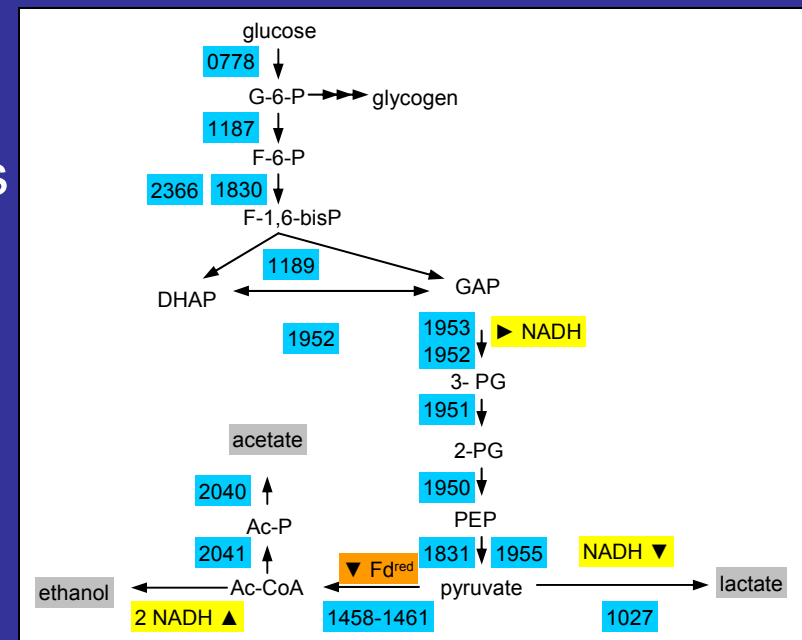
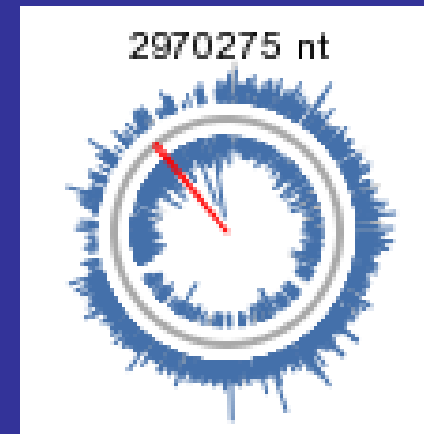


Higher tolerance H<sub>2</sub> than other thermophiles



# Csac Genome

- Proposed sequencing to JGI Spring 2006
  - Draft genome in 136 contigs Fall 2006
  - Sequence finished Feb 2007
- 2.97 Mb with a 35.3% GC content
- 2793 ORF's identified
  - > 60 GHs found in the genome
  - Contains > 177 ABC transporter genes
  - A fructose-specific PTS system
  - EM pathway
  - Non-oxidative PPP



# Csac Glycoside Hydrolases

Enzyme	GH family	MW (kDa)	Locus
pullulanase (pula)	13	95.7	Csac0671
$\beta$ -mannanase	5 and 44	146.9	Csac1077
cellulase (CelA)	9 and 48	193.7	Csac1076
cellulase (CelB)	10 and 5	117.6	Csac1078
$\beta$ -xylosidase (XynB)	39	56.4	Csac2404
endo-1,4- $\beta$ -xylanase	10	36.5	Csac2405
acetyl esterase (ORF2)	-	30.6	Csac2407
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CelA



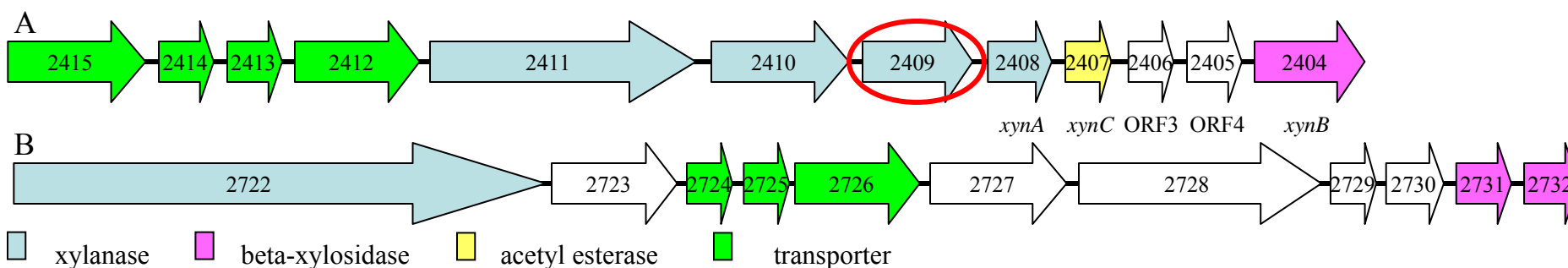
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CelA



## Xylanase Response Loci of Interest

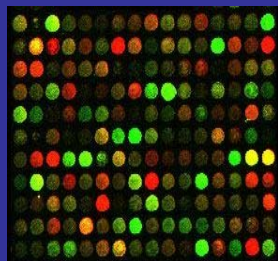
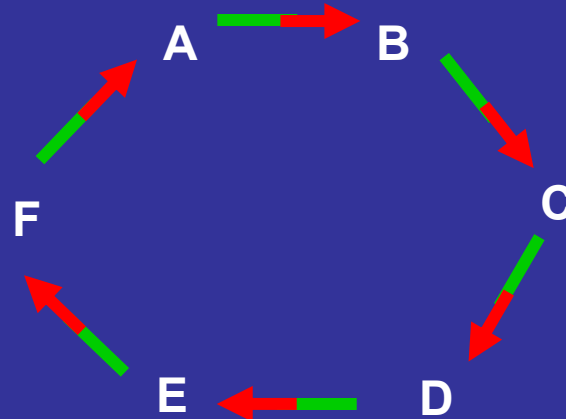


# Csac Transcriptomics

## Csac oligonucleotide spotted microarray

- 2793 ORFs represented by 60-mer probes
- 5 copies of each probe, randomized location

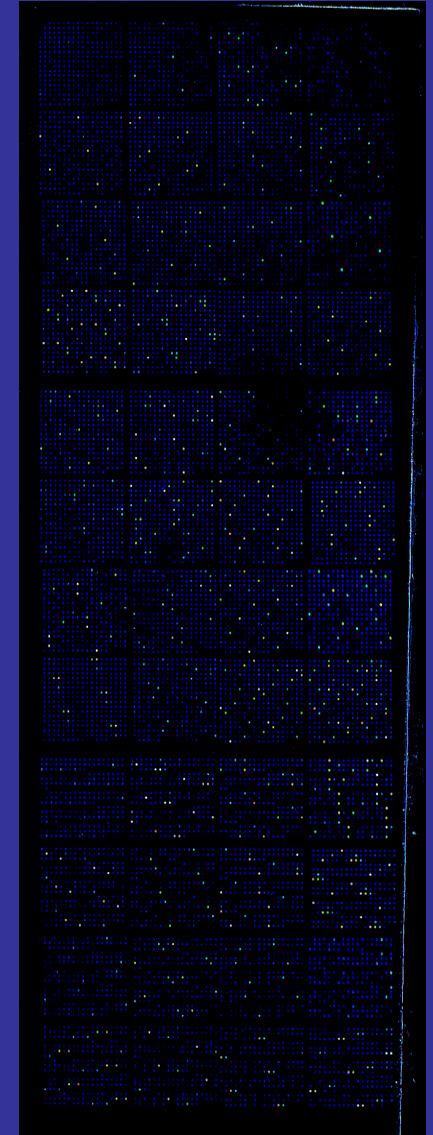
Loop  
experimental  
design



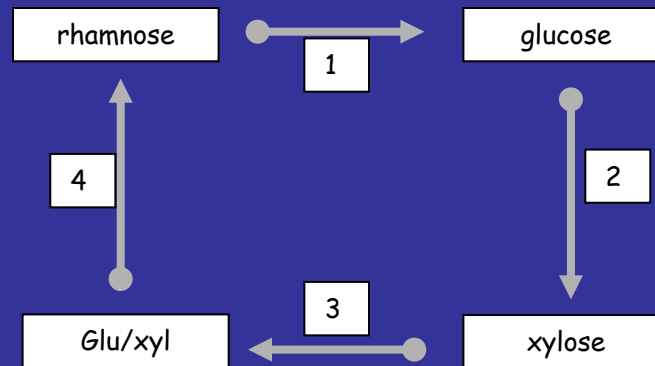
Data analysis:  
Mixed Model  
ANOVA



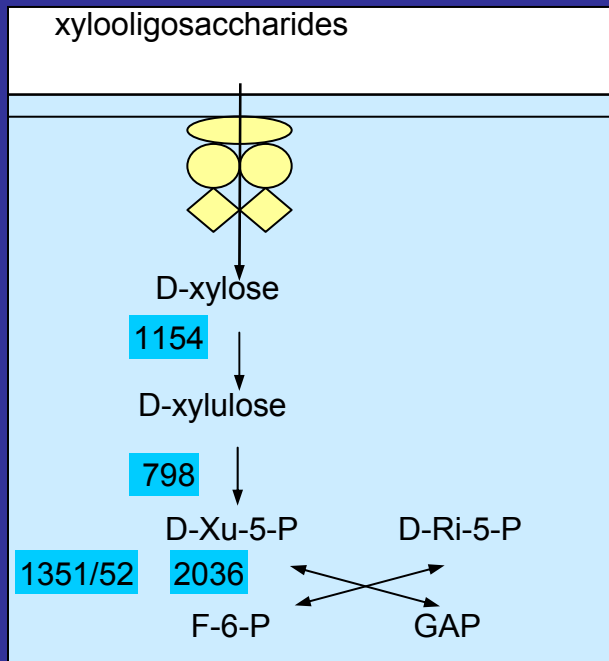
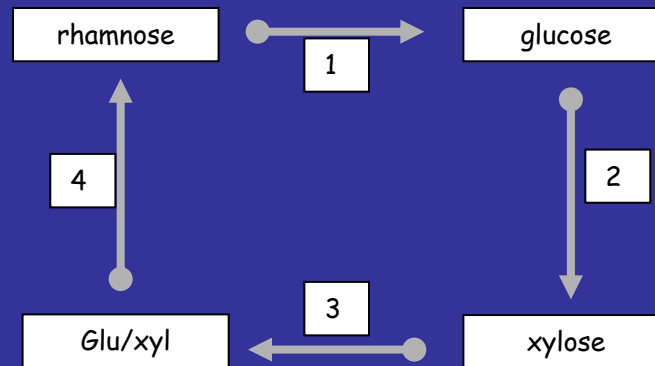
Transcriptional  
Response



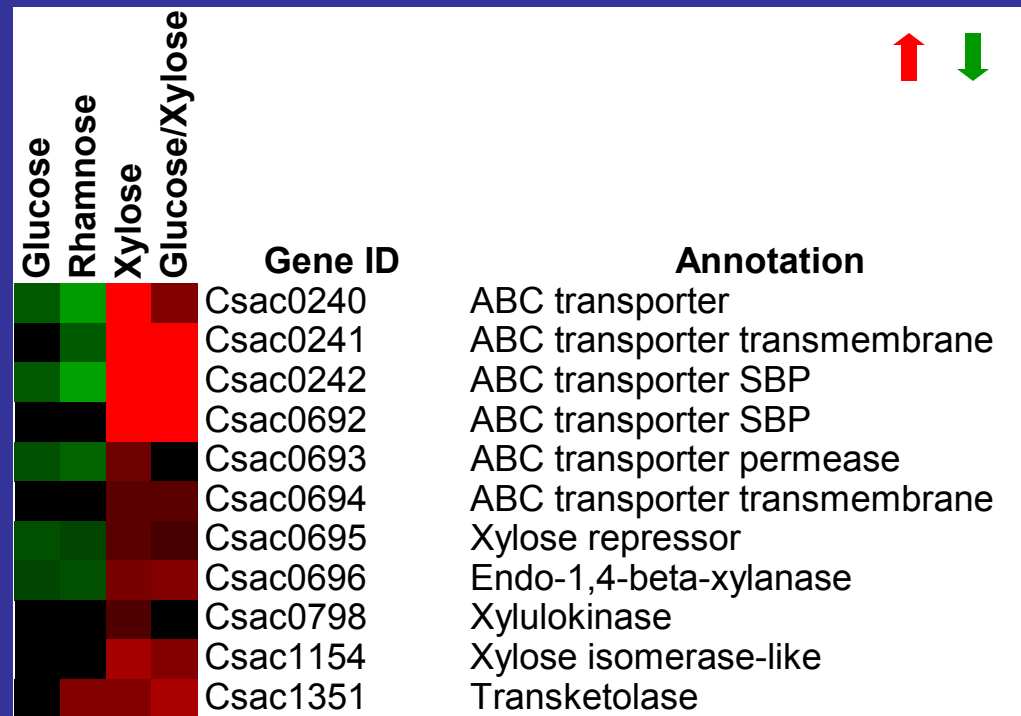
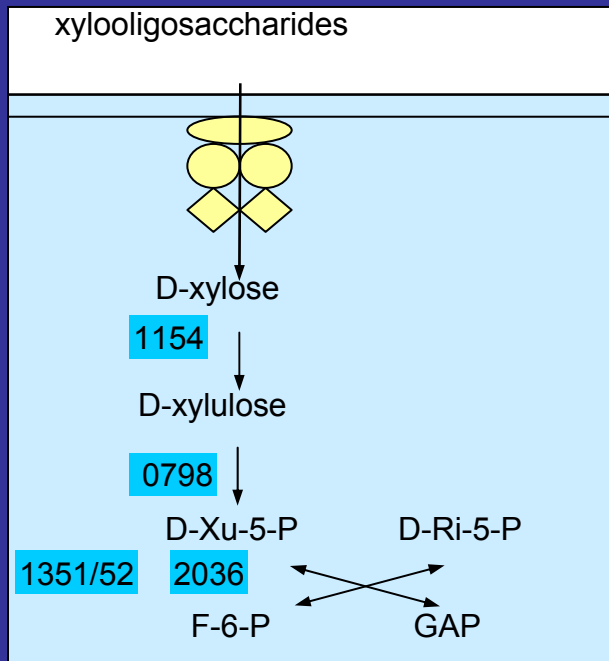
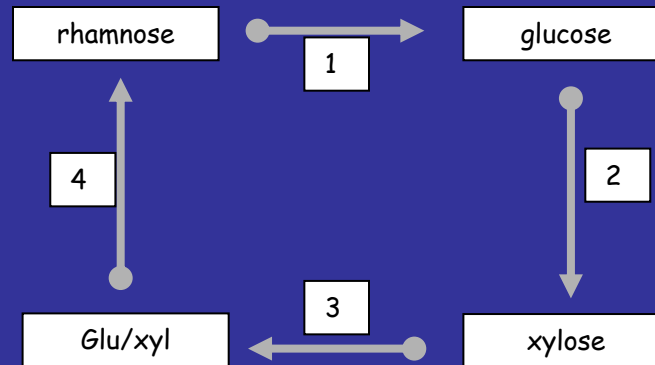
# Csac Xyl/Glu Co-fermentation



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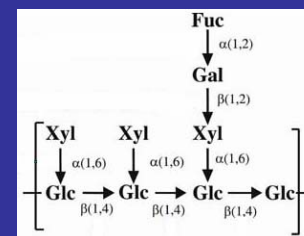
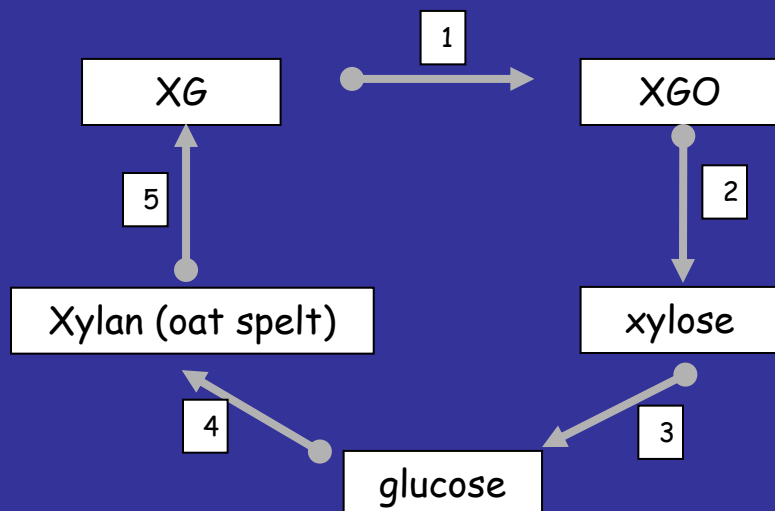
# Csac Xyl/Glu Co-fermentation





# XGO Utilization

xyloglucan (XG) links cellulose microfibrils together in plants

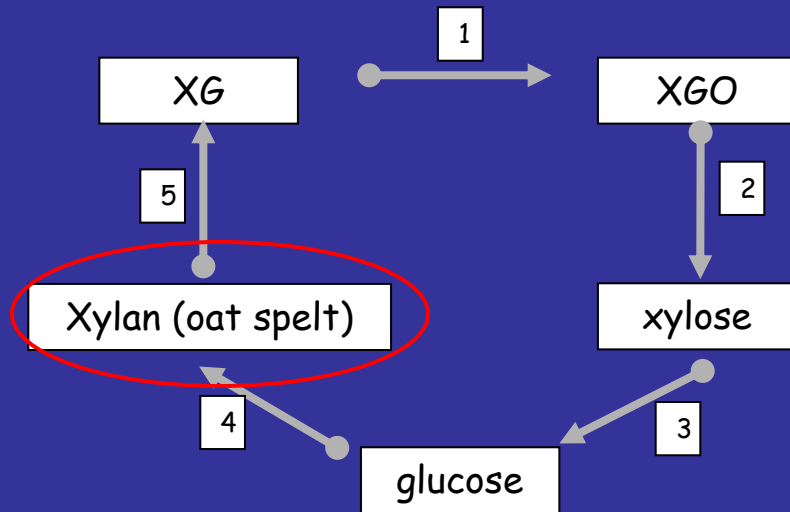


XG differently transcribed ORFs				
ORFs	XG vs XGO	XG vs xylose	XG vs glucose	XG vs xylan
↑	305	187	103	101
↓	438	181	73	39

Up-regulation of genes to degrade XG side chains and backbone

Fold changes of GH ORFs up-regulated on XG				
Gene	Annotation	XG vs XGO	XG vs glucose	XG vs xylose
Csac0689	pullulanase type I	2.6	2.1	2.3
Csac0779	acetyl xylan esterase	8.8	No change	No change
Csac0784	1,4- $\alpha$ -glucan branching enzyme	4.2	No change	No change
Csac1078	Endoglucanase	4.4	3.7	3.5
Csac1080	$\beta$ -mannanase	3.4	3.7	2.6
Csac1118	$\alpha$ -galactosidase	3.5	4.0	5.5

# Xylan Utilization



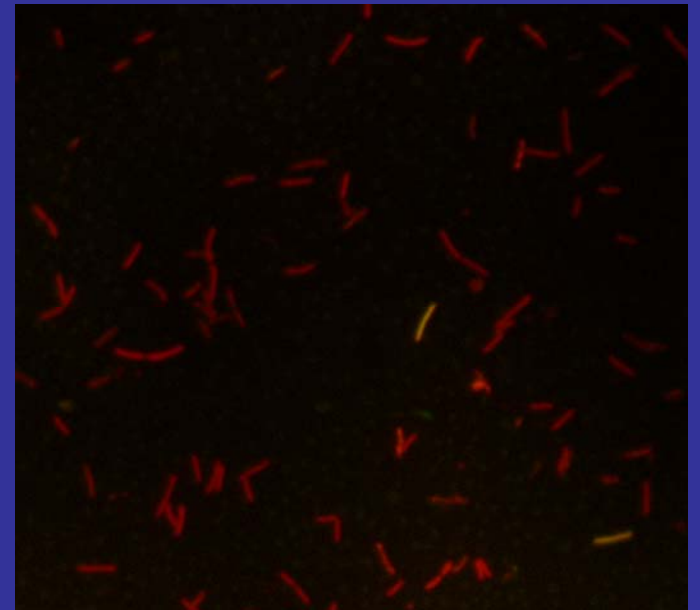
Xylan differently transcribed ORFs			
ORFs	xylan vs XGO	xylan vs xylose	xylan vs glucose
↑	231	172	168
↓	91	70	233

- Transcription of other hemicellulose degrading genes
  - $\beta$ -galactosidases,  $\beta$ -mannosidases, endoglucanases and pullulanases
- Constitutive expression of xylanases
  - Also found reported in fungi and the bacterium *Streptomyces cyaneus*

# Csac Biomass Degradar

Enzymes used synergistically to break down biomass material

Co-culture with a cellulose degrader to ferment sugars to biofuels



# Acknowledgments

## NSF, BESC (DOE) and GAANN



### **Collaborators:**

van der Oost lab at Wageningen University in the Netherlands

Ward lab at Genencor, Palo Alto CA

Adams lab at UGA, Athens GA

### **Kelly Group Members:**

#### **Current Members:**

Kate Auernik

Sarah Blumer-Schuetz, Ph.D.

Jaspreet Notey

Inci Ozdemir

Derrick Lewis

Samantha Zelin

J. Morgan Harris

Charlotte Cooper

Andrew Frock

Steven Gray

#### **Past Students and Post-Docs**